

Spatial-temporal Multicomponent Model in Surveillance Package

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Zhejiang Provincial Center for Disease Control and Prevention

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Introduction to surveillance package

Package:

- ▶ First version (0.9-1) published in the 21-Nov-2005, the maintainer is Michael Höhle, Stockholm University, Sweden
- ▶ Author-Homepage:
<http://staff.math.su.se/hoehle>
- ▶ Package-Homepage:
<https://cran.r-project.org/web/packages/surveillance/>

Motivation:

"To provide open source software for the temporal and spatio-temporal visualization and modelling of epidemic phenomena"

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Main features in surveillance package:

- ▶ Visualization of surveillance data and algorithm output
- ▶ Prospective detection of aberrations in routinely collected public health data
- ▶ Spatio-temporal point process intensity model
- ▶ SIR model on event history of a fixed population
- ▶ Spatial-temporal multivariate time-series model

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Spatio-temporal point process model

The spatial-temporal point process model in surveillance package also can be called as the spatial-temporal two-component conditional intensity function model.

- ▶ A novel point process model features so-called **self-excitement**, i.e. events promote the future evolution of the point process by producing "offspring" events.
- ▶ Modeling is based on an additive-multiplicative conditional intensity function continuous in spatial-temporal.
- ▶ The epidemic component is additionally generalised by **marks** and **covariates**.

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Model structure

Two-component conditional intensity function (TCCIF) model decomposes the disease risk additively into endemic and epidemic components. The basic framework of TCCIF is as followed:

$$\lambda^*(t, s) = h(t, s) + e^*(t, s) \quad (t > 0, s \in W)$$

$$h(t, s) = \exp(h_0^{\text{temp}}(t) + h_0^{\text{spat}}(s) + \tilde{\beta}\tilde{z}(t, s))$$

$$e^*(t, s) = \sum_{j \in I^*(t, s, \theta, \delta)} e^{nj} g(t - t_j) f(s - s_j)$$

$\lambda^*(t, s)$ represents the instantaneous rate or hazard in time t and location s ; $h(t, s)$ describes endemic pattern that captures exogenous factors; $e^*(t, s)$ is the realization of a spatial-temporal process with epidemic behavior.

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Specification of the epidemic component

- ▶ The epidemic component essentially provides a description of the infection pressure at a space-time location (t, s) caused by each infectious individual.
- ▶ The triggering function is factorised into separate effects of marks(e^{nj}), elapsed time($g(t - t_i)$) and relative location ($f(s - s_j)$).
- ▶ Marks function: $nj = \gamma_0 + \gamma * m_j$, a linear predictor. based on the vector of unpredictable marks $m^{--}j$.
- ▶ Spatial function: $f(s) = \exp\left(\frac{\|s\|^2}{2\sigma^2}\right)$, a radially symmetric kernel.
- ▶ Temporal function: $g(t) = e^{-\alpha t}$, a exponential temporal decay.

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Data structure: the epidataCS class

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- ▶ **events**: the core data set of point-referenced events as a "SpatialPointsDataFrame". The core data holds the following obligatory columns:
the event time; the length of the infectious period; the spatial influence radius and the enclosing tile of the space-time grid **stgrid**.
- ▶ **W**: "SpatialPolygons" object representing the observation region **W** containing the events.
- ▶ **stgrid** : data frame of covariates on a full space-time grid for the endemic component.
- ▶ **qmatrix**: square indicator matrix for possible transmission between event types.

Data Prepare: TCCIF

The epidataCS object is created by the function `as.epidataCS`. The argument of events, stgrid and W are obligatory.

- ▶ events: (`eps.t=14; eps.s=50`)

coordinates	gentle	age	date	dose	time	eps.t	eps.s	tile
(1438.51, 3308.586)	男	[0,0.667]	2013-12-31	1剂	369.8989	14	50	上城区
(1438.526, 3308.988)	女	[0,0.667]	2013-04-09	0剂	104.2396	14	50	上城区
(1436.068, 3309.064)	女	[0.667,14]	2013-04-21	2剂	115.5391	14	50	上城区
(1437.162, 3308.387)	女	[14,200]	2013-05-18	不详	143.2473	14	50	上城区
(1439.791, 3309.171)	女	[14,200]	2013-05-03	0剂	128.3214	14	50	上城区
(1435.749, 3306.159)	女	[0,0.667]	2013-10-02	0剂	280.4730	14	50	上城区

- ▶ stgrid: `dat.mn<-mutate(dat.mn,
start=rep(c(0,100,200,300),each=91),stop=start+100)`
- ▶ W: `dat.zj<- readShapePoly("SP_ID.shp",
proj4string=CRS("+proj=longlat +datum=WGS84
+no_defs +ellps=WGS84 +towgs84=0,0,0"))`

```
dat.epi<-as.epidataCS(events=dat.4,stgrid=dat.mn,W=dat.zj)
```

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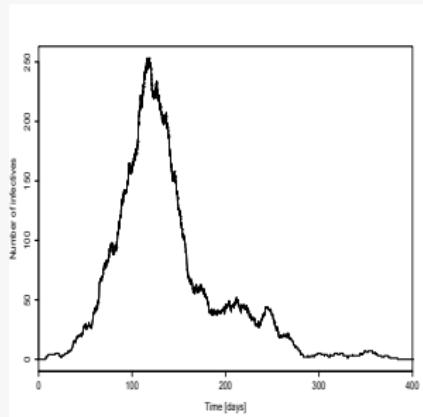
Data visualization: plot

► Plot in time:

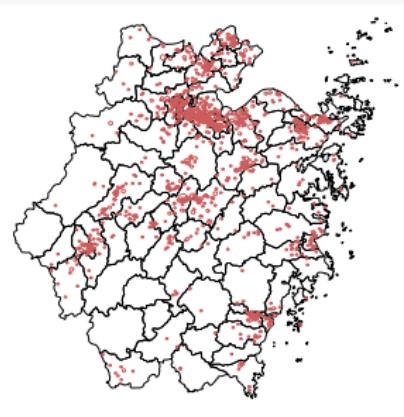
```
plot(as.stepfun(dat.epi), xlim=c(0,400), xaxs = "i", xlab =  
"Time [days]", ylab = "Number of infectives", main = "")
```

► Plot in space:

```
plot(dat.epi,"space",lwd = 2,points.args = list(pch = c(1,  
19), col = c("indianred", "darkblue")))
```



(a) Time



(b) Space

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Data visualization: animation

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Arguments in twinstim

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The function `twinstim` can be used to perform likelihood inference for conditional intensity model.

Main arguments in the `twinstim` include the `formulae of the endemic and epidemic predictors`, and the spatial and temporal interaction functions `siaf(f)` and `tiaf(g)`, respectively.

- ▶ Alternatives for spatial interaction:
constant; gaussian; powerlaw; powerlawL; step; student.
- ▶ Alternatives for temporal interaction:
constant; exponential; step

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Basic Model for TCCIF

- ▶ Data source: Measles data, population data and map data for the Zhejiang province, 2013.

- ▶ Codes for endemic component:

```
endemic<-addSeason2formula(~  
offset(log(popdt))+I(start/365-  
0.5),period=365,timevar="start")
```

Note: My data is only one year, so choose $1/2=0.5$;
the popdt is the population density of each district.

- ▶ Codes for the basic model(Without epidemic component):

```
imdefit<-twinstim(endemic=endemic,epidemic=~0,  
data=dat.epi)
```

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Update model - spatial interaction

Changing the `siaf` argument:

- ▶ Constant function [$f(s) = 1$]:

```
fit_sconstant <- update(imdefit, epidemic=~1,  
siaf=siaf.constant())
```

- ▶ Step function [$f(s) = \sum_{k=0}^K \exp(\alpha_k) I_k(|s|)$]:

```
fit_sstep <- update(imdefit, epidemic=~1,  
siaf=siaf.step(c(5,10)))
```

- ▶ Gaussian function [$f(s) = \exp\left(\frac{\|s\|^2}{2\sigma^2}\right)$]:

```
fit_sgaussian <- update(imdefit, epidemic=~1,  
siaf=siaf.gaussian())
```

- ▶ Power-law function [$f(s) = (|s| +)^{-d}$]:

```
fit_spowerlaw <- update(imdefit, epidemic=~1,  
siaf=siaf.powerlaw())
```

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Update model - temporal interaction

Changing the `tiaf` argument:

- ▶ Constant function [$g(t) = 1$]:

```
fit_tconstant <- update(imdefit, epidemic=~1,  
tiaf=tiaf.constant())
```

- ▶ Step function [$g(t) = \sum_{k=0}^K \exp(\alpha_k) I_k(t)$] :

```
fit_tstep <- update(imdefit,epidemic=~1,  
tiaf=tiaf.step(c(5,10)))
```

- ▶ Exponential function [$g(t) = \exp(-\alpha t)$] :

```
fit_texponential <- update(imdefit,epidemic=~1,  
tiaf=tiaf.exponential())
```

- ▶ Add covarites:

```
fit_covarites <- update(imdefit,epidemic=~ age+gentle)
```

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Endemic and epidemic effects

Estimated rate ratios (RR) and associated Wald confidence intervals (CI) for endemic and epidemic terms

	RR	95% CI	p-value
h.l(start/365 - 0.5)	0.121	0.04–0.33	<0.0001
h.sin(2 * pi * start/365)	2.463	1.95–3.11	<0.0001
h.cos(2 * pi * start/365)	0.797	0.57–1.11	0.18
e.age(0.667,14]	0.629	0.42–0.95	0.026
e.age(14,200]	0.988	0.78–1.25	0.92
e.gentle女	0.961	0.76–1.21	0.73

Interpretation: The results show a strong seasonality and a slow negative trend. Patients in the age group 8 month to 14 years cause approximately 0.629 times as many secondary infections as infants aged 0 to 8 month. **True or not?**

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- ▶ The coordinates must be defined in a planar coordinate reference system to enable Euclidean geometry.(spTransform function)
- ▶ The complex shapefile (i.e. isolated island) should be simplified (<http://mapshaper.org/>)
- ▶ All the point coordinates will be projected inside the stgrid.(Omit the case in oher region)
- ▶ Gaussian and powlaw method for spatial interaction will take many time.(Shorten the date range or use the parallel operation)

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History for univariate time-series

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Two main changes for univariate time-series:

- ▶ Log-linear Poisson regression model(Parameter-driven)

$$\eta_t = \alpha + \beta t + \sum_{s=1}^S (\gamma_s \sin(\psi_s t) + \delta_s \cos(\psi_s t))$$

Where, S is the number of harmonics to include and ψ_s are the Fourier frequencies.

- ▶ Branching process model with immigration(Parameter and observation-driven)

$$\mu_t = v\eta_t + \lambda y_{t-1}, 0 < \lambda < 1$$

Two parts for disease incidence: an endemic part with rate η_t and an epidemic part with conditional rate λy_{t-1} .

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Initial form for multivariate time-series

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- ▶ Multivariate time-series model is the extension of the univariate time-series model. For example, we might consider the number of cases in different age groups or different geographical regions.
- ▶ The simplest form doesn't consider the correlation between the different time-series, which only includes the **endemic component** and **autoregressive component**.
- ▶ The equation is as followed:

$$\mu_{i,t} = \nu \eta_{i,t} + \lambda y_{i,t-1}$$

$$\log v_{i,t} = \alpha + \beta t + \sum_{s=1}^S (\gamma_s \sin(\psi_s t) + \delta_s \cos(\psi_s t))$$

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General form for multivariate time-series

The disease incidence was divided into **endemic component**

($v_{i,t}\eta_{i,t}$), **autoregressive component** ($\lambda_{i,t}y_{i,t-1}$) and **epidemic component** ($\theta_{i,t} \sum_{i \neq j} (w_{i,j} Y_{i-1,j})$) in the following equation:

$$\mu_{i,t} = v_{i,t}\eta_{i,t} + \lambda_{i,t}y_{i,t-1} + \theta_{i,t} \sum_{i \neq j} (w_{i,j} Y_{i-1,j})$$

$$\log(v_{i,t}) = \alpha_0 + \alpha_i + z_{i,t}^T \alpha$$

$$\log(\lambda_{i,t}) = \gamma_0 + \gamma_i + \mu_{i,t}^T \gamma$$

$$\log(\theta_{i,t}) = \zeta_0 + \zeta_i + \beta t + \kappa_{i,t}^T \zeta$$

Where, α_0 , γ_0 and β_0 are the component-specific intercepts; α_i , γ_i and ζ_i are the random effects; β is a trend parameter; $z_{i,t}^T$, $\mu_{i,t}^T$ and $\kappa_{i,t}^T$ are the covariance matrix (i.e. vaccine coverage); $w_{i,j}$ is the spatial weight matrix.

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Advantages of the multivariate time-series model in surveillance package:

- ▶ **Spatial weight matrix**: Multiple ways to define the spatial interaction using the order-specific weights or powerlaw method.
- ▶ **Covariates effect**: covariate effects on the endemic or epidemic contributions to disease incidence.
- ▶ **Random effects**: useful if the districts exhibit heterogeneous incidence levels not explained by observed covariates.
- ▶ **Predictive model assessment**: one-step-ahead forecasts from competing models by proper scoring rules

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Data structure: The sts class

- ▶ **observed**: A $n \times m$ matrix of counts representing $y_{i,t}$.
- ▶ **start**: A vector of length two containing the origin of the time series as c(year, week).
- ▶ **freq**: A numeric specifying the period of the time series, i.e. 52 for weekly data, 12 for monthly data, etc.
- ▶ **epoch**: Object of class numeric or specifying the time of observation.
- ▶ **neighbourhood**: Symmetric matrix of size describing the neighbourhood structure.
- ▶ **populationFrac**: A matrix of population fractions (with dimensions $\text{dim}(\text{observed})$).

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- ▶ To import population and disease data into R one can use "read.table", "read.csv", "read_csv" or the RODBC database interface (Acess, Excel, SQL databases).

```
dat.final<-as.matrix(read.csv("disease.csv"))
populationFrac<-as.matrix(read.csv("populationFrac.csv"))
```

- ▶ The map data can be handed in the maptools package.

```
dat.zj<-readShapePoly("zhejiang3.shp")
measles_nb<-nbOrder(poly2adjmat(dat.zj),maxlag=10)
```

- ▶ An sts object is then created by the "**new**" function.

```
mmts <- new("sts",start=c(2013,1),freq=365,epoch= 1:365,
observed=dat.final, neighbourhood = measles_nb, map =
dat.zj, populationFrac = populationFrac)
```

Accessing sts objects

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- ▶ Matrix like accessing such as `mmts[1:60,]` or `mmts[1, "安吉县"]`.
- ▶ Functions such as `dim`, `nrow`, and `observed` et.al are also defined, i.e. `observed(mmmts)`
- ▶ The `slots` of sts objects, i.e. `mmts@observed`
- ▶ The time series can be aggregated temporally and spatially, i.e. `aggregate(mmmts, by = "unit")` or `aggregate(mmmts, by = "time")`
- ▶ Aggregation can also be of subsets. i.e. `aggregate(mmmts[, c("萧山区", "安吉县")], nfreq = 73)`

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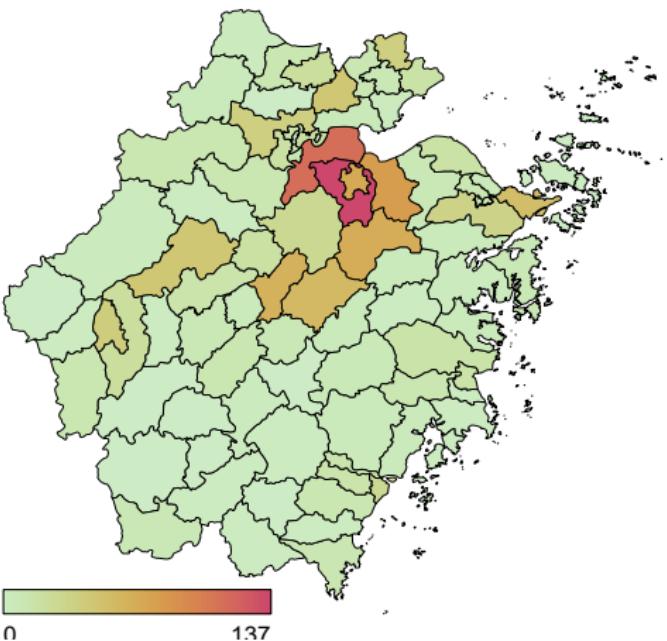
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Visualizing sts objects

The plot function provides an interface to several visual representations controlled by the **type** argument.

- ▶ `plot(mmcts, type = observed ~ 1|unit,labels=F)`



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Another ways to visualizing the sts objects:

- ▶ Plots with each containing the time series of one observational unit.

```
plot(mmts, type = observed ~ time | unit)
```

- ▶ The observations in x are aggregated over units and the resulting univariate time-series is plotted.

```
plot(mmts, type = observed ~ time)
```

- ▶ Animated maps for times.

```
plot(mmts,type=observed ~ 1 | unit * time)
```

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Example for Multivariate time-series model

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- ▶ **Data source:** Measles data, population data and map data for the Zhejiang province, 2013.
- ▶ **Covariate:** Floating children accounted for the proportion of local children, 2013.
- ▶ **Spatial weight matrix:** one-order(epidemic can only arrive from directly adjacent districts) and power-law method.
- ▶ **Model selection:** AIC for no random effect model and score rules for the random effect model.

Basic Model

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hhh4 or update function to creat the basic model:

```
mmts_bs <- list(end = list(f = addSeason2formula(~ 1+t, period  
= 365), offset = population(mmts)), ar = list(f = ~ 1), ne = list(f  
= ~ 1, weights = neighbourhood(mmts) == 1), family =  
"NegBin1")
```

```
mmts_basic <- hhh4(stsObj = mmts, control = mmts_bs)
```

control argument in the hhh4, which is a list containing several components:

- ▶ ar(Autoregressive component): f, offset, lag, weights, initial.
- ▶ ne(Epidemic component): f, offset, lag, weights, initial.
- ▶ end(Endemic component): f, offset, initial.

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Covariates effect

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Model include covariates effect:

► Covariates effect in the endemic component:

```
update(mmts_basic,end =list(f=update(  
formula(mmts_basic)$end, ~ .+ log(Sprop)), data =  
list(Sprop = Sprop))
```

► Covariates effect in the autoregressive component:

```
update(mmts_basic,ar =list(f=update(  
formula(mmts_basic)$ar, ~ .+ log(Sprop)), data =  
list(Sprop = Sprop))
```

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for Disease Control and

Change the spatial interaction

Spatial-temporal

Bing Zhang

Model with different ways to define the spatial weight matrix:

- ▶ Second-order model:

```
update(mmots_basic,ne = list(weights = W_np(maxlag =  
2)))
```

- ▶ Power-law model:

```
update(mmots_basic,ne = list(weights = W_powerlaw(maxlag  
= 5)))
```

The argument `maxlag` sets an upper bound for spatial interaction in terms of neighbourhood order. The available `maxlag` is 10 and you can use the codes `max(neighbourhood(mmots))` to look the `maxlag` in your spatial weight matrix.

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Random effects model

Spatial-temporal

Bing Zhang

The independent random effects in endemic, autoregressive and epidemic component:

- ▶

```
update(mmts_basic, end=list(  
  f=update(formula(mmts_basic)$end, ~ . + ri() - 1)),  
  ar=list(f=update(formula(mmts_basic)$ar, ~ . + ri() - 1)),  
  ne=list(f=update(formula(mmts_basic)$ne, ~ . + ri() - 1))))
```
- ▶ No correlation between the three intercepts in the default setting, but this is possible by specifying `ri(corr="all")` in the component formula.
- ▶ The implementation also supports a conditional autoregressive formulation for spatially correlated intercepts by using `ri(type="car")`.

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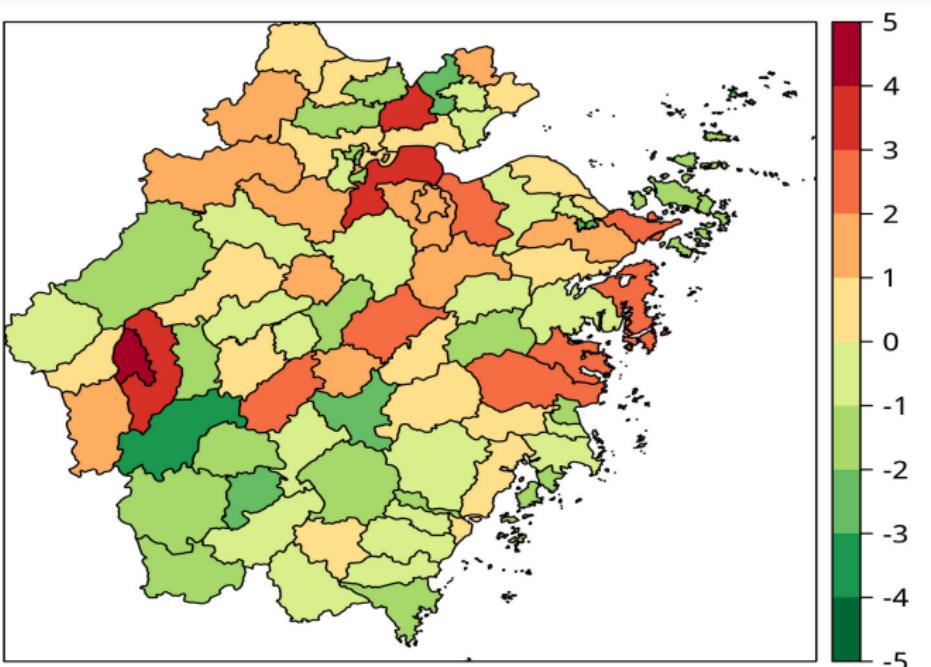
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Endemic component



Local risk of measles was high in Keqiao, Qujiang and Xiaoshan district with the endemic component at 4.06, 3.74 and 3.55, respectively.

Spatial-temporal

Bing Zhang

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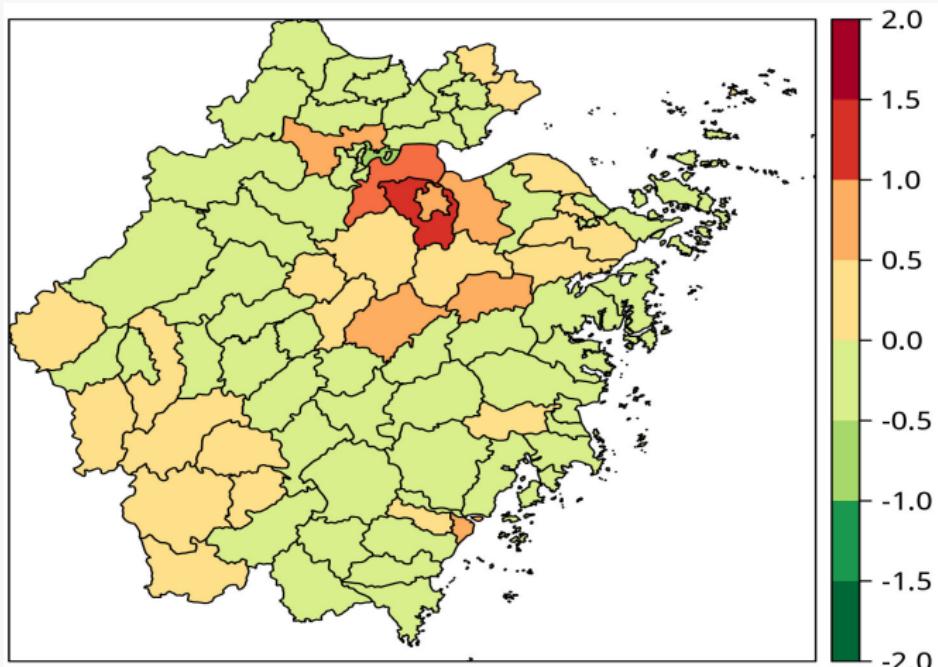
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Autoregressive component



Follow-up impact of the measles in Keqiao, Qujiang and Xiaoshan district were high with the autoregressive component at 4.06, 3.74 and 3.55, respectively.

Spatial-temporal

Bing Zhang

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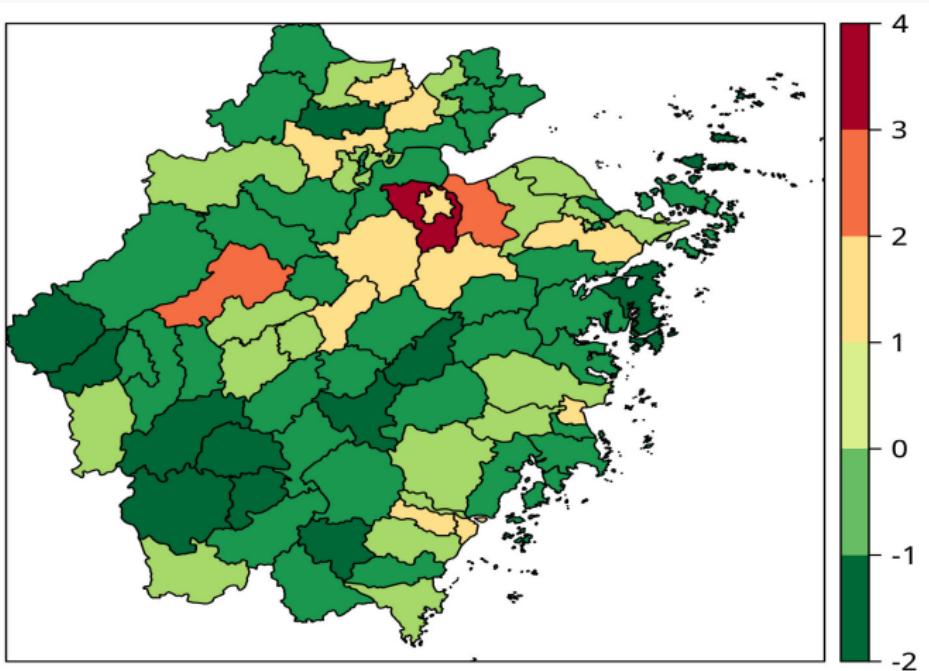
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Epidemic component



Impact of the epidemic from the nearby districts was large in Keqiao, Shangyu district and Jiande city with the epidemic component at 3.08, 2.54 and 2.21, respectively.

Spatial-temporal

Bing Zhang

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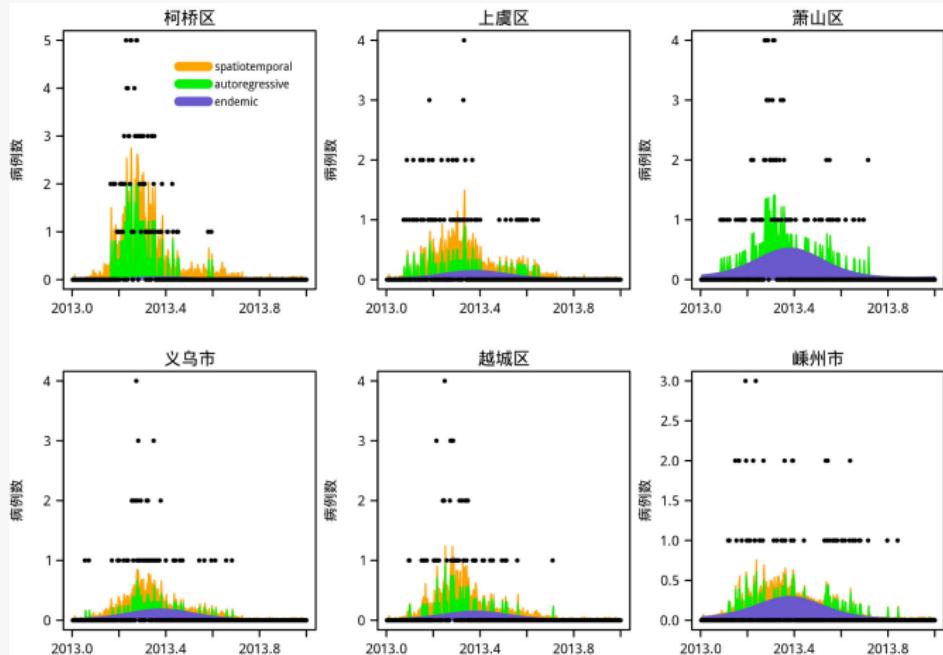
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Random effects



Local follow-up impact and impact from the nearby districts of the measles in Keqiao district were great. Local risk and local follow-up impact in Xiaoshan district were high.

Spatial-temporal

Bing Zhang

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Note for multivariate time-series model

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Bing Zhang

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- ▶ The tile in different dataset must keep consistent.(Check again and again)
- ▶ The position of the covariant was based on the ability of model fitting and the knowledge.
- ▶ The result will be not stable if the case counts are few.
(Large the analysis time)